ABSTRACT

Cancer research has experienced drastic revolutionizes in the past several years. Completion of the human genome project had signaled a new beginning for modern biology, where generating information both at the genetic and clinical levels is no longer the concern. Rather, how this information can be handled has become the major obstacle and barrier to progress. Intuitive approaches are no more feasible to cope with enormous and overwhelming data. The next big step will be to implement integrated modeling approaches to interrogate the massive amount of data being produced and extract useful and valuable answers, which could help physicians to make an appropriate therapeutic decision making. Notwithstanding decades of research, the ability to predict and treat metastatic breast cancer is extremely limited and inadequate (Reuben, Krishnamurthy, Woodward, & Cristofanilli, 2008). The intricacy to reliably prognosis the risk of breast cancer metastasis for individual patients stems from the fact that cancer is the result of a complex interplay between numerous factors, namely: cellular parameters–altered rates of cell proliferation, apoptosis, migration, adhesion, metabolism and mutation–and micro-environmental parameters–extracellular matrix (ECM) composition, angiogenesis, inflammation and proteases (Kaiser & Nasir, 2008). In addition, present breast cancer indices were discovered contain some restrictions in order to predict breast cancer metastasis, since patients with identical diagnostic and clinical prognostic profiles can have apparently diverse clinical outcome. This phenomenon is due to the missing genes cellular proliferations information in current breast cancer indices and a high reliance on a complex and inexact combination of clinical and histopathological data such as age, tumor size, estrogen and progesterone receptors, and lymph node involvement. Thus, these indices were notified to provide misleading results as it mainly group molecularly distinct patients into alike clinical classes generally based on morphological of disease. Although clinical and histopathological data are relevance to predict breast cancer metastasis but gene cellular proliferation also is essential information that needs to be taken into consideration. These existing restrictions reveal the need to apply more rational approaches to minimize the morbidity and mortality of metastatic cancer. Due to the overwhelming flow of data currently being produced in the biomedical sciences and complex interaction between clinical and gene information in breast cancer invasion and metastasis, an integrated modeling approach is described here. Bayesian network has been proposed as a method to develop an integrated model for breast cancer prognosis. Bayesian network is a well known technique in biomedical and bioinformatics and offers several advantages such as it inherently model the uncertainty in the data. It is also a successful combination between probability theory and graph theory. Furthermore, this technique allows different strategies and data types to be combined.